



SEQUENCE LISTING

<110> FEDER, J. N.
MINTIER, G.
RAMANATHAN, C. S.
HAWKEN, D. R.

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,
EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES

<130> D0041NP

<140> 09/965,536

<141> 2001-09-26

<150> 60/235,713

<151> 2000-09-27

<150> 60/261,781

<151> 2001-01-16

<150> 60/306,605

<151> 2001-07-19

<150> 60/310,436

<151> 2001-08-03

<160> 61

<170> PatentIn Ver. 2.1

<210> 1

<211> 2214

<212> DNA

<213> Homo sapiens

<400> 1

```
atgttctttc tacttcattt catcgttctg atcaatgtca aagattttgc actgactcaa 60
ggtagcatga tcttccttc atgccaaaaa ggatattttc cctgtgggaa tcttaccaag 120
tgcttacccc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggccggacgaa 180
gagaactgtg gtgacactag tggatgggcg accatatattg gcacagtgc tggaaatgct 240
aacagcgtgg ccttaacaca ggagtgtttt ctaaaacagt atccacaatg ctgtgactgc 300
aaagaaactg aattggaatg tgtaaattgt gacttaaagt ctgtgccgat gatttctaac 360
aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttccaga taaagttttc 420
atcaaataca caaaacttaa aaagatatatt cttcagcata attgcattag acacatatcc 480
aggaaagcat tttttggatt atgtaatctg caaatattat atctcaacca caactgcatc 540
acaaccctca gacctggaat attcaaagac ttacatcagc taacttggct aattctagat 600
gacaatccaa taaccagaat ttcacagcgc ttgttttacgg gattaaattc cttgtttttc 660
```

ctgtctatgg ttaataacta cttagaagct cttcccaagc agatgtgtgc ccaaagcct 720
 caactcaact ggggtgattt ggaaggcaat agaataaagt atctcacaaa ttctacgttt 780
 ctgtcgtgcg attcgtcac agtgcgtttt tttaaagac ttgaaactgc atctgtctag caatacgata 840
 gagaagacat tttcttcatt ttttaagac cagtttgaaa gtcttaaca accatgtct 900
 acggagctat cactcacct tcacaagaac gattccaaat ataacacac gaatgttcca accatgtct 960
 tccaatcctc ttatgtatct caaaaacttt cgatactgct cctatgtccc ccatgtcga 1020
 ctgacctgg aaaggataga cggcattttt cgtactgctt cctatgtccc ccatgtcga 1080
 aatcttttc cctgtacgga agtgcgtttt attactgctt ttgtctttg ttggcatttt cgatataaaa 1140
 atctgtatgc cctgtacgga agtgcgtttt attactgctt ttgtctttg ttggcatttt cgatataaaa 1200
 ctcagaatat ttgtctgggt tatagctttt acaactcacg ctatgtccc ccatgtcga 1260
 ggcagagat ctttcattaa ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1320
 tggtgtgctg agtatcagaa gtatgccttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1380
 taccgagggc agtatcagaa gtatgccttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1440
 atggggttcc tggtcatttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1500
 ttggagaagt tctcattttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1560
 acctcagtc tctcattttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1620
 tggaataaag attattttg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1680
 tatgacaaa cagaagatat ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1740
 aactgtctg cttttctcat ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1800
 aaaacggct tgcagaccac ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1860
 aatcgtttt tttttatccg ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1920
 aaaatcctt cagtttaacag ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 1980
 ttttaaggaca agttgaaaca ggtgtgtttt cgtgtggttg agagcgtgca ctactgact 2040
 aaaaaaaa gtttatctac atccattgtg tggatagagg ggaatcaat tttcaaaatt 2100
 ggggttttga aaaaaataac acttgagac agtataatga aaccagtttc ctg 2160

<210> 2

<211> 737

<212> PRT

<213> Homo sapiens

<400> 2

Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp Phe

1

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln	85	90	95
Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu	100	105	110
Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys	115	120	125
Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr	130	135	140
Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser	145	150	155
Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn	165	170	175
His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His	180	185	190
Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser	195	200	205
Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val	210	215	220
Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro	225	230	235
Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr	245	250	255
Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro	260	265	270
Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys	275	280	285
Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser	290	295	300
Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser	305	310	315
Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys	325	330	335

Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
 340 345 350
 Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
 355 360 365
 Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
 370 375 380
 Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
 385 390 395 400
 Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
 405 410 415
 Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
 420 425 430
 His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
 435 440 445
 Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
 450 455 460
 Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu
 465 470 475 480
 Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu
 485 490 495
 Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
 500 505 510
 Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
 515 520 525
 Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp
 530 535 540
 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
 545 550 555 560
 Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
 565 570 575
 Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
 580 585 590

Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu
 595 600 605
 Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe
 610 615 620
 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val
 625 630 635 640
 Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
 645 650 655
 Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
 660 665 670
 Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
 675 680 685
 Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
 690 695 700
 Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
 705 710 715 720
 Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val
 725 730 735

Ser

<210> 3
 <211> 17
 <212> DNA
 <213> Homo sapiens

<400> 3
 ccacgcgtcc gattaca

17

<210> 4
 <211> 1026
 <212> DNA
 <213> Homo sapiens

<400> 4
 caatcatttt ggatcactgg acttttcagt gactacctaa aacaggggac agctttttgga 60

```

agatgacatc tgcaatgctt ttcattcttta ccaacggcaa gccttttctgc acagagagca 120
cagcagaatg gctcctgtca ctgcattcca atggcagctg tactatctac caaccgtgct 180
gaggacagca ccaaagggtt ctctcctcac cccacatgcc tgaaaagcac atgtgaattc 240
gtgtatagtg ggctgaggtg cagctgatct ctagctaate aacacaaccc accaacaat 300
gaccacaggt tggcactgtg tggctcttca catcgggttg cactgtccat gaaatagaaa 360
cactcacaac atctgattcc agtgtggcca taataacaga aatctaacaa ctctttcctt 420
gccttttcaa tatcaaataa aaccatcagc atcctgctgg attgatagca aaggatttcc 480
aaaatattca tctacccgaa gtccctcctt gtgaaggccg gtggagtagc cactttgaaa 540
acagaacttc caaccagggt accatgtcta acctatgacc agagagtcac actgatgaag 600
cctcatacca tttgcctttt ggattttatt taatatcaga agagatgaat tcttaagata 660
tttttctgaa ggttgcccag ggcacaaaca aattggacac tttcactgct aaaaagtaca 720
ctttaatatt cttaaagtat aatttcttta gagcagtatc cctattgctg gcaagttctg 780
ctttcataaa atatgcagat aagaagtgtt aaatgggatt caagaattat ggttttattt 840
gggactgttt gcatactcac aatgggtttt ttctcattgt ttttaacaaa aaagcaatga 900
agtttggggt ggttttttga aaacgaaact gaaaaaaatt atatgtgaaa atgagaactg 960
ggtaaataaa atttatattt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaag                                           1026

```

<210> 5

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 5

```

atgttctttc tacttcattt catcgttctg atcaatgtca aagattttgc actgactcaa 60
ggtagcatga tctactcctt atgccaaaaa ggatattttc cctgtgggaa tcttaccag 120
tgcttacccc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180
gagaactgtg gtgacactag tggatgggag accatatttg gcacagtgc tggaaatgct 240
aacagcgtgg ccttaacaca ggagtgtttt ctaaaacagt atccacaatg ctgtgactgc 300
aaagaaactg aattggaatg tgtaaattgt gacttaaagt ctgtgccgat gatttctaac 360
aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttcaga taaagttttc 420
atcaaataca caaaacttaa aaagatatct cttcagcata attgcattag acacatatcc 480
aggaaagcat tttttggatt atgtaatctg caaatattaa ttctagatga caatccaata 540
accagaattt cacagcgtt gtttacggga ttaaattcct tgtttttcct gtctatgggt 600
aataactact tagaagctct tcccaagcag atgtgtgccc aaatgcctca actcaactgg 660
gtggatttgg aaggcaatag aataaagtat ctacacaaatt ctacgtttct gtcgtgcgat 720
tcgctcacag tgctgtttct gcctagaaat caaattgggt ttgttccaga gaagacattt 780
tcttcattaa aaaatttagg agaactggat ctgtctagca atacgataac ggagctatca 840
cctcaccttt ttaaagactt gaagcttcta caaaagctga acctgtcatc caatcctctt 900
atgtatcttc acaagaacca gtttgaaagt cttaaacaac ttcagtctct agacctggaa 960
aggatagaga ttccaaatat aaacacacga atgtttcaac ccatgaagaa tctttctcac 1020
atatttttca aaaactttcg atactgtctc tatgtctccc atgtccgaat atgtatgcc 1080
ttgacggacg gcatttcttc atttgaggac ctcttggtta acaatatact cagaatatatt 1140
gtctgggtta tagctttcat tacctgcttt ggaaatcttt ttgtcattgg catgagatct 1200
ttcattaaag ctgaaaatac aactcacgct atgtccatca aaatcctttg ttgtgctgat 1260
tgctgatgg gtgtttactt gttctttgtt ggcattttcg atataaaata ccgagggcag 1320
tatcagaagt atgccttgct gtggatggag agcgtgcagt gccgcctcat ggggttctct 1380

```

```

gccatgctgt ccaccgaagt ctctgttctg ctactgacct acttgacttt ggagaagttc 1440
ctggtcattg tcttcccctt cagtaacatt cgacctggaa aacggcagac ctcagtcac 1500
ctcatttgca tctggatggc gggattttta atagctgtaa ttccattttg gaataaggat 1560
tattttggaa acttttatgg gaaaaatgga gtatgtttcc cactttatta tgaccaaaca 1620
gaagatattg gaagcaaagg gtattctctt ggaattttcc taggtgtgaa cttgctggct 1680
tttctcatca ttgtgttttc ctatattact atgttctgtt ccattcaaaa aaccgccttg 1740
cagaccacag aagtaaggaa ttgttttgga agagaggtgg ctgttgcaaa tcgtttcttt 1800
tttatagtgt tctctgatgc catctgctgg attcctgtat ttgtagttaa aatcctttcc 1860
ctcttcgggg tggaatatcc agacacaatg acttcctgga tagtgatttt tttccttcca 1920
gttaacagtg ctttgaatcc aatcctctat actctcacia ccaacttttt taaggacaag 1980
ttgaaacagc tgctgcacia acatcagagg aaatcaattt tcaaaattaa aaaaaaagt 2040
ttatctacat ccattgtgtg gatagaggac tcctcttccc tgaaacttgg ggttttgaac 2100
aaaataacac ttggagacag tataatgaaa ccagtttcct ag 2142

```

<210> 6

<211> 713

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp Phe
  1                      5                      10                      15

```

```

Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr
      20                      25                      30

```

```

Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
      35                      40                      45

```

```

Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
      50                      55                      60

```

```

Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
      65                      70                      75                      80

```

```

Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
      85                      90                      95

```

```

Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
      100                      105                      110

```

```

Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
      115                      120                      125

```

```

Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
      130                      135                      140

```

Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
 145 150 155 160
 Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp
 165 170 175
 Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn
 180 185 190
 Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro
 195 200 205
 Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu
 210 215 220
 Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp
 225 230 235 240
 Ser Leu Thr Val Leu Phe Leu Pro Arg Asn Gln Ile Gly Phe Val Pro
 245 250 255
 Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu Asp Leu Ser
 260 265 270
 Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys
 275 280 285
 Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His
 290 295 300
 Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu
 305 310 315 320
 Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys
 325 330 335
 Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala
 340 345 350
 Pro His Val Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe
 355 360 365
 Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val Ile
 370 375 380
 Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg Ser
 385 390 395 400

Phe	Ile	Lys	Ala	Glu	Asn	Thr	Thr	His	Ala	Met	Ser	Ile	Lys	Ile	Leu	405	410	415
Cys	Cys	Ala	Asp	Cys	Leu	Met	Gly	Val	Tyr	Leu	Phe	Phe	Val	Gly	Ile	420	425	430
Phe	Asp	Ile	Lys	Tyr	Arg	Gly	Gln	Tyr	Gln	Lys	Tyr	Ala	Leu	Leu	Trp	435	440	445
Met	Glu	Ser	Val	Gln	Cys	Arg	Leu	Met	Gly	Phe	Leu	Ala	Met	Leu	Ser	450	455	460
Thr	Glu	Val	Ser	Val	Leu	Leu	Leu	Thr	Tyr	Leu	Thr	Leu	Glu	Lys	Phe	465	470	475
Leu	Val	Ile	Val	Phe	Pro	Phe	Ser	Asn	Ile	Arg	Pro	Gly	Lys	Arg	Gln	485	490	495
Thr	Ser	Val	Ile	Leu	Ile	Cys	Ile	Trp	Met	Ala	Gly	Phe	Leu	Ile	Ala	500	505	510
Val	Ile	Pro	Phe	Trp	Asn	Lys	Asp	Tyr	Phe	Gly	Asn	Phe	Tyr	Gly	Lys	515	520	525
Asn	Gly	Val	Cys	Phe	Pro	Leu	Tyr	Tyr	Asp	Gln	Thr	Glu	Asp	Ile	Gly	530	535	540
Ser	Lys	Gly	Tyr	Ser	Leu	Gly	Ile	Phe	Leu	Gly	Val	Asn	Leu	Leu	Ala	545	550	555
Phe	Leu	Ile	Ile	Val	Phe	Ser	Tyr	Ile	Thr	Met	Phe	Cys	Ser	Ile	Gln	565	570	575
Lys	Thr	Ala	Leu	Gln	Thr	Thr	Glu	Val	Arg	Asn	Cys	Phe	Gly	Arg	Glu	580	585	590
Val	Ala	Val	Ala	Asn	Arg	Phe	Phe	Phe	Ile	Val	Phe	Ser	Asp	Ala	Ile	595	600	605
Cys	Trp	Ile	Pro	Val	Phe	Val	Val	Lys	Ile	Leu	Ser	Leu	Phe	Arg	Val	610	615	620
Glu	Ile	Pro	Asp	Thr	Met	Thr	Ser	Trp	Ile	Val	Ile	Phe	Phe	Leu	Pro	625	630	635
Val	Asn	Ser	Ala	Leu	Asn	Pro	Ile	Leu	Tyr	Thr	Leu	Thr	Thr	Asn	Phe	645	650	655

Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln Arg Lys Ser
660 665 670

Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile Val Trp Ile
675 680 685

Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr Leu
690 695 700

Gly Asp Ser Ile Met Lys Pro Val Ser
705 710

<210> 7

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 5'
primer

<400> 7

aatggaatta cagctattaa aaatcccgcc atccagatgc aaatgaggat gactgaggtc 60
tgccgttttc caggtcgaat 80

<210> 8

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
oligos

<400> 8

aagcagatgt gtgccc aaat g 21

<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
oligos

<400> 9
 ggtgaggtga tagttccggt atcg

24

<210> 10
 <211> 1115
 <212> PRT
 <213> *Lymnaea stagnalis*

<400> 10
 Met Ala Thr Met Ser Gly Thr Thr Ile Val Cys Leu Ile Tyr Leu Thr
 1 5 10 15
 Thr Met Leu Gly Asn Ser Gln Gly Val Asn Leu Lys Ile Glu Ser Pro
 20 25 30
 Ser Pro Pro Thr Leu Cys Ser Val Glu Gly Thr Phe His Cys Asp Asp
 35 40 45
 Gly Met Leu Gln Cys Val Leu Met Gly Ser Lys Cys Asp Gly Val Ser
 50 55 60
 Asp Cys Glu Asn Gly Met Asp Glu Ser Val Glu Thr Cys Gly Cys Leu
 65 70 75 80
 Gln Ser Glu Phe Gln Cys Asn His Thr Thr Cys Ile Asp Lys Ile Leu
 85 90 95
 Arg Cys Asp Arg Asn Asp Asp Cys Ser Asn Gly Leu Asp Glu Arg Glu
 100 105 110
 Cys Asp Ile Tyr Ile Cys Pro Leu Gly Thr His Val Lys Trp His Asn
 115 120 125
 His Phe Cys Val Pro Arg Asp Lys Gln Cys Asp Phe Leu Asp Asp Cys
 130 135 140
 Gly Asp Asn Ser Asp Glu Lys Ile Cys Glu Arg Arg Glu Cys Val Ala
 145 150 155 160
 Thr Glu Phe Lys Cys Asn Asn Ser Gln Cys Val Ala Phe Gly Asn Leu
 165 170 175
 Cys Asp Gly Leu Val Asp Cys Val Asp Gly Ser Asp Glu Asp Gln Val
 180 185 190
 Ala Cys Asp Ser Asp Lys Tyr Phe Gln Cys Ala Glu Gly Ser Leu Ile

195					200					205						
Lys	Lys	Glu	Phe	Val	Cys	Asp	Gly	Trp	Val	Asp	Cys	Lys	Leu	Thr	Phe	
210					215					220						
Ala	Asp	Glu	Leu	Asn	Cys	Lys	Leu	Cys	Asp	Glu	Asp	Asp	Phe	Arg	Cys	
225					230					235					240	
Ser	Asp	Thr	Arg	Cys	Ile	Gln	Lys	Ser	Asn	Val	Cys	Asp	Gly	Tyr	Cys	
245					250					255						
Asp	Cys	Lys	Thr	Cys	Asp	Asp	Glu	Glu	Val	Cys	Ala	Asn	Asn	Thr	Tyr	
260					265					270						
Gly	Cys	Pro	Met	Asp	Thr	Lys	Tyr	Met	Cys	Arg	Ser	Ile	Tyr	Gly	Glu	
275					280					285						
Pro	Arg	Cys	Ile	Asp	Lys	Asp	Asn	Val	Cys	Asn	Met	Ile	Asn	Asp	Cys	
290					295					300						
Arg	Asp	Gly	Asn	Val	Gly	Thr	Asp	Glu	Tyr	Tyr	Cys	Ser	Asn	Asp	Ser	
305					310					315					320	
Glu	Cys	Lys	Asn	Phe	Gln	Ala	Ala	Met	Gly	Phe	Phe	Tyr	Cys	Pro	Glu	
325					330					335						
Glu	Arg	Cys	Leu	Ala	Lys	His	Leu	Tyr	Cys	Asp	Leu	His	Pro	Asp	Cys	
340					345					350						
Ile	Asn	Gly	Glu	Asp	Glu	Gln	Ser	Cys	Leu	Ala	Pro	Pro	Lys	Cys	Ser	
355					360					365						
Gln	Asp	Glu	Phe	Gln	Cys	His	His	Gly	Lys	Cys	Ile	Pro	Ile	Ser	Lys	
370					375					380						
Arg	Cys	Asp	Ser	Val	His	Asp	Cys	Val	Asp	Trp	Ser	Asp	Glu	Met	Asn	
385					390					395					400	
Cys	Glu	Asn	His	Gln	Cys	Ala	Ala	Asn	Met	Lys	Ser	Cys	Leu	Ser	Gly	
405					410					415						
His	Cys	Ile	Glu	Glu	His	Lys	Trp	Cys	Asn	Phe	His	Arg	Glu	Cys	Pro	
420					425					430						
Asp	Gly	Ser	Asp	Glu	Lys	Asp	Cys	Asp	Pro	Arg	Pro	Val	Cys	Glu	Ala	
435					440					445						
Asn	Gln	Phe	Arg	Cys	Lys	Asn	Gly	Gln	Cys	Ile	Asp	Pro	Leu	Gln	Val	

450		455		460															
Cys	Val	Lys	Gly	Asp	Lys	Tyr	Asp	Gly	Cys	Ala	Asp	Gln	Ser	His	Leu				
465					470					475					480				
Ile	Asn	Cys	Ser	Gln	His	Ile	Cys	Leu	Glu	Gly	Gln	Phe	Arg	Cys	Arg				
				485					490						495				
Lys	Ser	Phe	Cys	Ile	Asn	Gln	Thr	Lys	Val	Cys	Asp	Gly	Thr	Val	Asp				
			500					505					510						
Cys	Leu	Gln	Gly	Met	Trp	Asp	Glu	Asn	Asn	Cys	Arg	Tyr	Trp	Cys	Pro				
	515						520					525							
His	Gly	Gln	Ala	Ile	Cys	Gln	Cys	Glu	Gly	Val	Thr	Met	Asp	Cys	Thr				
	530					535					540								
Gly	Gln	Lys	Leu	Lys	Glu	Met	Pro	Val	Gln	Gln	Met	Glu	Glu	Asp	Leu				
545					550				555						560				
Ser	Lys	Leu	Met	Ile	Gly	Asp	Asn	Leu	Leu	Asn	Leu	Thr	Ser	Thr	Thr				
			565					570						575					
Phe	Ser	Ala	Thr	Tyr	Tyr	Asp	Lys	Val	Thr	Tyr	Leu	Asp	Leu	Ser	Arg				
			580					585					590						
Asn	His	Leu	Thr	Glu	Ile	Pro	Ile	Tyr	Ser	Phe	Gln	Asn	Met	Trp	Lys				
	595						600					605							
Leu	Thr	His	Leu	Asn	Leu	Ala	Asp	Asn	Asn	Ile	Thr	Ser	Leu	Lys	Asn				
	610					615					620								
Gly	Ser	Leu	Leu	Gly	Leu	Ser	Asn	Leu	Lys	Gln	Leu	His	Ile	Asn	Gly				
625					630					635				640					
Asn	Lys	Ile	Glu	Thr	Ile	Glu	Glu	Asp	Thr	Phe	Ser	Ser	Met	Ile	His				
			645					650					655						
Leu	Thr	Val	Leu	Asp	Leu	Ser	Asn	Gln	Arg	Leu	Thr	His	Val	Tyr	Lys				
		660						665					670						
Asn	Met	Phe	Lys	Gly	Leu	Lys	Gln	Ile	Thr	Val	Leu	Asn	Ile	Ser	Arg				
	675						680					685							
Asn	Gln	Ile	Asn	Ser	Ile	Asp	Asn	Gly	Ala	Phe	Asn	Asn	Leu	Ala	Asn				
	690					695						700							
Val	Arg	Leu	Ile	Asp	Leu	Ser	Gly	Asn	Val	Ile	Lys	Asp	Ile	Gly	Gln				

705		710		715		720
Lys Val Phe Met Gly Leu Pro Arg Leu Val Glu Leu Lys Thr Asp Ser						
	725		730		735	
Tyr Arg Phe Cys Cys Leu Ala Pro Glu Gly Val Lys Cys Ser Pro Lys						
	740		745		750	
Gln Asp Glu Phe Ser Ser Cys Glu Asp Leu Met Ser Asn His Val Leu						
	755		760		765	
Arg Val Ser Ile Trp Val Leu Gly Val Ile Ala Leu Val Gly Asn Phe						
	770		775		780	
Val Val Ile Phe Trp Arg Val Arg Asp Phe Arg Gly Gly Lys Val His						
785		790		795		800
Ser Phe Leu Ile Thr Asn Leu Ala Ile Gly Asp Phe Leu Met Gly Val						
	805		810		815	
Tyr Leu Leu Ile Ile Ala Thr Ala Asp Thr Tyr Tyr Arg Gly Val Tyr						
	820		825		830	
Ile Ser His Asp Glu Asn Trp Lys Gln Ser Gly Leu Cys Gln Phe Ala						
	835		840		845	
Gly Phe Val Ser Thr Phe Ser Ser Glu Leu Ser Val Leu Thr Leu Ser						
	850		855		860	
Thr Ile Thr Leu Asp Arg Leu Ile Cys Ile Leu Phe Pro Leu Arg Arg						
865		870		875		880
Thr Arg Leu Gly Leu Arg Gln Ala Ile Ile Val Met Ser Cys Ile Trp						
	885		890		895	
Val Leu Val Phe Leu Leu Ala Val Leu Pro Leu Leu Gly Phe Ser Tyr						
	900		905		910	
Phe Glu Asn Phe Tyr Gly Arg Ser Gly Val Cys Leu Ala Leu His Val						
	915		920		925	
Thr Pro Asp Arg Arg Pro Gly Trp Glu Tyr Ser Val Gly Val Phe Ile						
	930		935		940	
Leu Leu Asn Leu Leu Ser Phe Val Leu Ile Ala Ser Ser Tyr Leu Trp						
945		950		955		960
Met Phe Ser Val Ala Lys Lys Thr Arg Ser Ala Val Arg Thr Ala Glu						

	965		970		975										
Ser	Lys	Asn	Asp	Asn	Ala	Met	Ala	Arg	Arg	Met	Thr	Leu	Ile	Val	Met
			980						985					990	
Thr	Asp	Phe	Cys	Cys	Trp	Val	Pro	Ile	Ile	Val	Leu	Gly	Phe	Val	Ser
			995				1000						1005		
Leu	Ala	Gly	Ala	Arg	Ala	Asp	Asp	Gln	Val	Tyr	Ala	Trp	Ile	Ala	Val
		1010					1015					1020			
Phe	Val	Leu	Pro	Leu	Asn	Ser	Ala	Thr	Asn	Pro	Val	Ile	Tyr	Thr	Leu
1025					1030					1035					1040
Ser	Thr	Ala	Pro	Phe	Leu	Gly	Asn	Val	Arg	Lys	Arg	Ala	Asn	Arg	Phe
					1045					1050				1055	
Arg	Lys	Ser	Phe	Ile	His	Ser	Phe	Thr	Gly	Asp	Thr	Lys	His	Ser	Tyr
			1060						1065					1070	
Val	Asp	Asp	Gly	Thr	Thr	His	Ser	Tyr	Cys	Glu	Lys	Lys	Ser	Pro	Tyr
		1075						1080					1085		
Arg	Gln	Leu	Glu	Leu	Lys	Arg	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Pro	Pro
		1090					1095						1100		
Met	Tyr	Tyr	Asn	Thr	Glu	Leu	His	Ser	Asp	Ser					
1105						1110				1115					

<210> 11
 <211> 692
 <212> PRT
 <213> RAT

<400> 11															
Met	Ala	Leu	Leu	Leu	Val	Ser	Leu	Leu	Ala	Phe	Leu	Gly	Thr	Gly	Ser
1					5				10					15	
Gly	Cys	His	His	Trp	Leu	Cys	His	Cys	Ser	Asn	Arg	Val	Phe	Leu	Cys
					20			25					30		
Gln	Asp	Ser	Lys	Val	Thr	Glu	Ile	Pro	Thr	Asp	Leu	Pro	Arg	Asn	Ala
		35						40					45		
Ile	Glu	Leu	Arg	Phe	Val	Leu	Thr	Lys	Leu	Arg	Val	Ile	Pro	Lys	Gly
		50					55					60			

Ser	Phe	Ala	Gly	Phe	Gly	Asp	Leu	Glu	Lys	Ile	Glu	Ile	Ser	Gln	Asn	65	70	75	80
Asp	Val	Leu	Glu	Val	Ile	Glu	Ala	Asp	Val	Phe	Ser	Asn	Leu	Pro	Lys	85	90	95	
Leu	His	Glu	Ile	Arg	Ile	Glu	Lys	Ala	Asn	Asn	Leu	Leu	Tyr	Ile	Asn	100	105	110	
Pro	Glu	Ala	Phe	Gln	Asn	Leu	Pro	Ser	Leu	Arg	Tyr	Leu	Leu	Ile	Ser	115	120	125	
Asn	Thr	Gly	Ile	Lys	His	Leu	Pro	Ala	Val	His	Lys	Ile	Gln	Ser	Leu	130	135	140	
Gln	Lys	Val	Leu	Leu	Asp	Ile	Gln	Asp	Asn	Ile	Asn	Ile	His	Ile	Val	145	150	155	160
Ala	Arg	Asn	Ser	Phe	Met	Gly	Leu	Ser	Phe	Glu	Ser	Val	Ile	Leu	Trp	165	170	175	
Leu	Ser	Lys	Asn	Gly	Ile	Glu	Glu	Ile	His	Asn	Cys	Ala	Phe	Asn	Gly	180	185	190	
Thr	Gln	Leu	Asp	Glu	Leu	Asn	Leu	Ser	Asp	Asn	Asn	Asn	Leu	Glu	Glu	195	200	205	
Leu	Pro	Asn	Asp	Val	Phe	Gln	Gly	Ala	Ser	Gly	Pro	Val	Ile	Leu	Asp	210	215	220	
Ile	Ser	Arg	Thr	Lys	Val	His	Ser	Leu	Pro	Asn	His	Gly	Leu	Glu	Asn	225	230	235	240
Leu	Lys	Lys	Leu	Arg	Ala	Arg	Ser	Thr	Tyr	Arg	Leu	Lys	Lys	Leu	Pro	245	250	255	
Asn	Leu	Asp	Lys	Phe	Val	Thr	Leu	Met	Glu	Ala	Ser	Leu	Thr	Tyr	Pro	260	265	270	
Ser	His	Cys	Cys	Ala	Phe	Ala	Asn	Leu	Lys	Arg	Gln	Ile	Ser	Glu	Leu	275	280	285	
His	Pro	Ile	Cys	Asn	Lys	Ser	Ile	Leu	Arg	Gln	Asp	Ile	Asp	Asp	Met	290	295	300	
Thr	Gln	Ile	Gly	Asp	Gln	Arg	Val	Ser	Leu	Ile	Asp	Asp	Glu	Pro	Ser	305	310	315	320

Tyr Gly Lys Gly Ser Asp Met Met Tyr Asn Glu Phe Asp Tyr Asp Leu
 325 330 335
 Cys Asn Glu Val Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala Phe
 340 345 350
 Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu Ile
 355 360 365
 Trp Phe Ile Ser Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu Val
 370 375 380
 Val Leu Thr Thr Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu Met
 385 390 395 400
 Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu Leu
 405 410 415
 Ile Ala Ser Val Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr Ala
 420 425 430
 Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr
 435 440 445
 Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu
 450 455 460
 Glu Arg Trp His Thr Ile Thr His Ala Met Gln Leu Glu Cys Lys Val
 465 470 475 480
 Gln Leu Arg His Ala Ala Ser Val Met Val Leu Gly Trp Thr Phe Ala
 485 490 495
 Phe Ala Ala Ala Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys
 500 505 510
 Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln Leu
 515 520 525
 Tyr Val Met Ala Leu Leu Val Leu Asn Val Leu Ala Phe Val Val Ile
 530 535 540
 Cys Gly Cys Tyr Thr His Ile Tyr Leu Thr Val Arg Asn Pro Thr Ile
 545 550 555 560
 Val Ser Ser Ser Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Thr Leu
 565 570 575

Ile	Phe	Thr	Asp	Phe	Leu	Cys	Met	Ala	Pro	Ile	Ser	Phe	Phe	Ala	Ile	580	585	590
Ser	Ala	Ser	Leu	Lys	Val	Pro	Leu	Ile	Thr	Val	Ser	Lys	Ala	Lys	Ile	595	600	605
Leu	Leu	Val	Leu	Phe	Tyr	Pro	Ile	Asn	Ser	Cys	Ala	Asn	Pro	Phe	Leu	610	615	620
Tyr	Ala	Ile	Phe	Thr	Lys	Asn	Phe	Arg	Arg	Asp	Phe	Phe	Ile	Leu	Leu	625	630	635
Ser	Lys	Phe	Gly	Cys	Tyr	Glu	Met	Gln	Ala	Gln	Ile	Tyr	Arg	Thr	Glu	645	650	655
Thr	Ser	Ser	Ala	Thr	His	Asn	Phe	His	Ala	Arg	Lys	Ser	His	Cys	Ser	660	665	670
Ser	Ala	Pro	Arg	Val	Thr	Asn	Ser	Tyr	Val	Leu	Val	Pro	Leu	Asn	His	675	680	685
Ser	Ser	Gln	Asn													690		

<210> 12
 <211> 688
 <212> PRT
 <213> Rattus norvegicus

Met	Ala	Leu	Leu	Leu	Val	Ser	Leu	Leu	Ala	Phe	Leu	Gly	Thr	Gly	Ser	1	5	10	15
Gly	Cys	His	His	Trp	Leu	Cys	His	Cys	Ser	Asn	Arg	Val	Phe	Leu	Cys	20	25	30	
Gln	Asp	Ser	Lys	Val	Thr	Glu	Ile	Pro	Thr	Asp	Leu	Pro	Arg	Asn	Ala	35	40	45	
Ile	Glu	Leu	Arg	Phe	Val	Leu	Thr	Lys	Leu	Arg	Val	Ile	Pro	Lys	Gly	50	55	60	
Ser	Phe	Ala	Gly	Phe	Gly	Asp	Leu	Glu	Lys	Ile	Glu	Ile	Ser	Gln	Asn	65	70	75	80
Asp	Val	Leu	Glu	Val	Ile	Glu	Ala	Asp	Val	Phe	Ser	Asn	Leu	Pro	Lys	85	90	95	

Leu	His	Glu	Ile	Arg	Ile	Glu	Lys	Ala	Asn	Asn	Leu	Leu	Tyr	Ile	Asn	100	105	110
Pro	Glu	Ala	Phe	Gln	Asn	Leu	Pro	Ser	Leu	Arg	Tyr	Leu	Leu	Ile	Ser	115	120	125
Asn	Thr	Gly	Ile	Lys	His	Leu	Pro	Ala	Val	His	Lys	Ile	Gln	Ser	Leu	130	135	140
Gln	Lys	Val	Leu	Leu	Asp	Ile	Gln	Asp	Asn	Ile	Asn	Ile	His	Ile	Val	145	150	155
Ala	Arg	Asn	Ser	Phe	Met	Gly	Leu	Ser	Phe	Glu	Trp	Leu	Ser	Lys	Asn	165	170	175
Gly	Ile	Glu	Glu	Ile	His	Asn	Cys	Ala	Phe	Asn	Gly	Thr	Gln	Leu	Asp	180	185	190
Glu	Leu	Asn	Leu	Ser	Asp	Asn	Asn	Asn	Leu	Glu	Glu	Leu	Pro	Asn	Asp	195	200	205
Val	Phe	Gln	Gly	Ala	Ser	Gly	Pro	Val	Ile	Leu	Asp	Ile	Ser	Arg	Thr	210	215	220
Lys	Val	His	Ser	Leu	Pro	Asn	His	Gly	Leu	Glu	Asn	Leu	Lys	Lys	Leu	225	230	235
Arg	Ala	Arg	Ser	Thr	Tyr	Arg	Trp	Lys	Lys	Leu	Pro	Asn	Leu	Asp	Lys	245	250	255
Phe	Val	Thr	Leu	Met	Glu	Ala	Ser	Leu	Thr	Tyr	Pro	Ser	His	Cys	Cys	260	265	270
Ala	Phe	Ala	Asn	Leu	Lys	Arg	Gln	Ile	Ser	Glu	Leu	His	Pro	Ile	Cys	275	280	285
Asn	Lys	Ser	Ile	Leu	Arg	Gln	Asp	Ile	Asp	Asp	Met	Thr	Gln	Ile	Gly	290	295	300
Asp	Gln	Arg	Val	Ser	Leu	Ile	Asp	Asp	Glu	Pro	Ser	Tyr	Gly	Lys	Gly	305	310	315
Ser	Asp	Met	Met	Tyr	Asn	Glu	Phe	Asp	Tyr	Asp	Leu	Cys	Asn	Glu	Val	325	330	335
Val	Asp	Val	Thr	Cys	Ser	Pro	Lys	Pro	Asp	Ala	Phe	Asn	Pro	Cys	Glu	340	345	350

Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser
 355 360 365
 Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu Val Val Leu Thr Thr
 370 375 380
 Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala
 385 390 395 400
 Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val
 405 410 415
 Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln
 420 425 430
 Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser
 435 440 445
 Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His
 450 455 460
 Thr Ile Thr His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His
 465 470 475 480
 Ala Ala Ser Val Met Val Leu Gly Trp Thr Phe Ala Phe Ala Ala Ala
 485 490 495
 Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys
 500 505 510
 Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ala
 515 520 525
 Leu Leu Val Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr
 530 535 540
 Thr His Ile Tyr Leu Thr Val Arg Asn Pro Thr Ile Val Ser Ser Ser
 545 550 555 560
 Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Thr Leu Ile Phe Thr Asp
 565 570 575
 Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ser Leu
 580 585 590
 Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys Ile Leu Leu Val Leu
 595 600 605

Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe
610 615 620

Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly
625 630 635 640

Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Ala
645 650 655

Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser Ser Ala Pro Arg
660 665 670

Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His Ser Ser Gln Asn
675 680 685

<210> 13

<211> 687

<212> PRT

<213> Equus asinus

<400> 13

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Gln Val Cys His Tyr Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Leu Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Lys Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asn Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asp
100 105 110

His Asp Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser

115	120	125
Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu		
130	135	140
Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val		
145	150	155 160
Glu Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Met Ile Leu Arg		
	165	170 175
Leu Ser Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly		
	180	185 190
Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu		
	195	200 205
Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp		
	210	215 220
Ile Ser Gly Thr Arg Ile His Ser Leu Pro Asn Tyr Gly Leu Glu Asn		
225	230	235 240
Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro		
	245	250 255
Ser Leu Glu Lys Phe Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro		
	260	265 270
Ser His Cys Cys Ala Phe Ala Asn Trp Arg Gln Gln Thr Ser Glu Leu		
	275	280 285
Gln Thr Thr Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Met Thr		
	290	295 300
Gln Ala Arg Gly Glu Arg Val Ser Leu Ala Glu Asp Asp Glu Ser Met		
305	310	315 320
Met Tyr Ser Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp Val		
	325	330 335
Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met		
	340	345 350
Gly Tyr Asp Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala		
	355	360 365
Ile Thr Gly Asn Ile Ile Val Leu Val Ile Leu Ile Thr Ser Gln Tyr		

370		375		380
Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp				
385		390		400
Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val Asp Ile His				
	405		410	415
Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala				
	420		425	430
Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Gly Ser Glu Leu Ser				
	435		440	445
Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr				
	450		455	460
His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His Ala Ala Ser				
465		470		480
Val Met Leu Val Gly Trp Ile Phe Gly Phe Gly Val Gly Leu Leu Pro				
	485		490	495
Ile Phe Gly Ile Ser Thr Tyr Met Lys Val Ser Ile Cys Leu Pro Met				
	500		505	510
Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val				
	515		520	525
Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Thr His Ile				
	530		535	540
Tyr Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Ser Asp Thr				
545		550		560
Lys Ile Ala Lys Arg Met Gly Ile Leu Ile Phe Thr Asp Phe Leu Cys				
	565		570	575
Met Ala Pro Ile Ser Phe Phe Gly Ile Ser Ala Ser Leu Lys Val Ala				
	580		585	590
Leu Ile Thr Val Ser Lys Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro				
	595		600	605
Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn				
610		615		620
Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly Cys Tyr Glu				

625		630		635		640									
Met	Gln	Ala	Gln	Thr	Tyr	Arg	Thr	Glu	Thr	Ser	Ser	Thr	Gly	His	Ile
				645					650					655	
Ser	His	Pro	Lys	Asn	Gly	Pro	Cys	Pro	Pro	Thr	Pro	Arg	Val	Thr	Asn
			660					665					670		
Gly	Ala	Asn	Cys	Thr	Leu	Val	Pro	Leu	Ser	His	Leu	Ala	Gln	Asn	
		675					680					685			
<210> 14															
<211> 693															
<212> PRT															
<213> CHICKEN															
<400> 14															
Met	Ser	Leu	Gly	Leu	Thr	Cys	Leu	Leu	Ile	Leu	Leu	Ala	Ser	Cys	Ser
1				5					10					15	
Gly	Cys	Gln	His	His	Thr	Cys	Leu	Cys	Glu	Gly	Arg	Ile	Phe	Ile	Cys
			20					25					30		
Gln	Glu	Ile	Lys	Val	Val	Gln	Leu	Pro	Arg	Asp	Ile	Pro	Thr	Asn	Ala
		35					40						45		
Thr	Glu	Leu	Arg	Phe	Val	Leu	Thr	Lys	Met	Arg	Val	Ile	Pro	Lys	Gly
		50					55					60			
Ala	Phe	Thr	Gly	Leu	His	Asp	Leu	Glu	Lys	Ile	Glu	Ile	Ser	Gln	Asn
65					70					75					80
Asp	Ala	Leu	Glu	Ile	Ile	Glu	Gly	Asn	Val	Phe	Ser	Ser	Leu	Pro	Lys
				85					90					95	
Leu	His	Glu	Ile	Arg	Ile	Glu	Lys	Ala	Asn	Lys	Leu	Met	Lys	Ile	Asp
			100					105					110		
Gln	Asp	Ala	Phe	Gln	His	Leu	Pro	Ser	Leu	Arg	Tyr	Leu	Leu	Ile	Ser
		115						120				125			
Asn	Thr	Gly	Leu	Ser	Phe	Leu	Pro	Val	Val	His	Lys	Val	His	Ser	Phe
		130					135				140				
Gln	Lys	Val	Leu	Leu	Asp	Val	Gln	Asp	Asn	Ile	His	Ile	Arg	Thr	Ile
145					150					155					160

Glu	Arg	Asn	Thr	Phe	Met	Gly	Leu	Ser	Ser	Glu	Ser	Val	Ile	Leu	Arg	165	170	175	
Leu	Asn	Lys	Asn	Gly	Ile	Gln	Glu	Ile	Lys	Asp	His	Ala	Phe	Asn	Gly	180	185	190	
Thr	Cys	Leu	Asp	Glu	Leu	Asn	Leu	Ser	Asp	Asn	Tyr	Asn	Leu	Glu	Lys	195	200	205	
Leu	Pro	Glu	Lys	Val	Phe	Gln	Gly	Ala	Ile	Gly	Pro	Val	Val	Leu	Asp	210	215	220	
Ile	Ser	Arg	Thr	Arg	Ile	Ser	Phe	Leu	Pro	Ser	His	Gly	Leu	Glu	Phe	225	230	235	240
Ile	Lys	Lys	Leu	Arg	Ala	Arg	Ser	Thr	Tyr	Lys	Leu	Lys	Lys	Leu	Pro	245	250	255	
Asp	Val	Asn	Lys	Phe	Arg	Ser	Leu	Ile	Glu	Ala	Asn	Phe	Thr	Tyr	Pro	260	265	270	
Ser	His	Cys	Cys	Ala	Phe	Thr	Asn	Arg	Lys	Thr	Gln	Asn	Thr	Glu	Phe	275	280	285	
Tyr	Pro	Ile	Cys	Ser	Met	Ser	Pro	Ala	Lys	Gln	Asp	Leu	Gly	Glu	Gln	290	295	300	
Thr	Gly	Lys	Arg	Lys	His	Arg	Arg	Ser	Ala	Ala	Glu	Asp	Tyr	Ile	Ser	305	310	315	320
His	Tyr	Gly	Thr	Arg	Phe	Gly	Pro	Val	Glu	Asn	Glu	Phe	Asp	Tyr	Gly	325	330	335	
Leu	Cys	Asn	Glu	Val	Val	Asp	Phe	Val	Cys	Ser	Pro	Lys	Pro	Asp	Ala	340	345	350	
Phe	Asn	Pro	Cys	Glu	Asp	Ile	Met	Gly	Tyr	Asn	Val	Leu	Arg	Val	Leu	355	360	365	
Ile	Trp	Phe	Ile	Asn	Ile	Leu	Ala	Ile	Thr	Gly	Asn	Thr	Thr	Val	Leu	370	375	380	
Ile	Ile	Leu	Ile	Ser	Ser	Gln	Tyr	Lys	Leu	Thr	Val	Pro	Arg	Phe	Leu	385	390	395	400
Met	Cys	Asn	Leu	Ala	Phe	Ala	Asp	Leu	Cys	Ile	Gly	Ile	Tyr	Leu	Leu	405	410	415	

Phe	Ile	Ala	Ser	Val	Asp	Ile	Gln	Thr	Lys	Ser	Arg	Tyr	Tyr	Asn	Tyr	420	425	430
Ala	Ile	Asp	Trp	Gln	Thr	Gly	Ala	Gly	Cys	Asn	Ala	Ala	Gly	Phe	Phe	435	440	445
Thr	Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr	Thr	Leu	Thr	Val	Ile	Thr	450	455	460
Leu	Glu	Arg	Trp	His	Thr	Ile	Thr	Tyr	Ala	Met	Gln	Leu	Asn	Arg	Lys	465	470	475 480
Val	Arg	Leu	Arg	His	Ala	Val	Ile	Ile	Met	Val	Phe	Gly	Trp	Met	Phe	485	490	495
Ala	Phe	Thr	Val	Ala	Leu	Leu	Pro	Ile	Phe	Gly	Ile	Ser	Ser	Tyr	Met	500	505	510
Lys	Val	Ser	Ile	Cys	Leu	Pro	Met	His	Ile	Glu	Thr	Pro	Phe	Ser	Gln	515	520	525
Ala	Tyr	Val	Ile	Phe	Leu	Leu	Val	Leu	Asn	Val	Leu	Ala	Phe	Val	Ile	530	535	540
Ile	Cys	Ile	Cys	Tyr	Ile	Cys	Ile	Tyr	Phe	Thr	Val	Arg	Asn	Pro	Asn	545	550	555 560
Val	Ile	Ser	Ser	Asn	Ser	Asp	Thr	Lys	Ile	Ala	Lys	Arg	Met	Ala	Ile	565	570	575
Leu	Ile	Phe	Thr	Asp	Phe	Leu	Cys	Met	Ala	Pro	Ile	Ser	Phe	Phe	Ala	580	585	590
Ile	Ser	Ala	Ser	Leu	Arg	Val	Pro	Leu	Ile	Thr	Val	Ser	Lys	Ser	Lys	595	600	605
Ile	Leu	Leu	Val	Leu	Phe	Tyr	Pro	Ile	Asn	Ser	Cys	Ala	Asn	Pro	Phe	610	615	620
Leu	Tyr	Ala	Ile	Phe	Thr	Lys	Thr	Phe	Arg	Arg	Asp	Phe	Phe	Ile	Leu	625	630	635 640
Leu	Ser	Lys	Phe	Gly	Cys	Cys	Glu	Met	Gln	Ala	Gln	Ile	Tyr	Arg	Thr	645	650	655
Glu	Thr	Ser	Ser	Ser	Ala	His	Asn	Phe	His	Thr	Arg	Asn	Gly	His	Tyr	660	665	670

Pro Thr Ala Ser Lys Asn Ser Asp Gly Thr Ile Tyr Ser Leu Val Pro
 675 680 685

Leu Asn His Leu Asn
 690

<210> 15
 <211> 676
 <212> PRT
 <213> Callithrix jacchus

<400> 15
 Met Lys Gln Pro Leu Leu Ala Leu Gln Leu Leu Lys Leu Leu Leu Leu
 1 5 10 15

Leu Leu Leu Pro Leu Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Arg
 20 25 30

Cys Cys Pro Glu Pro Cys Asn Cys Thr Pro Asp Gly Ala Leu Arg Cys
 35 40 45

Pro Gly Pro Gly Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro
 50 55 60

Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile
 65 70 75 80

Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn
 85 90 95

Ala Phe Asp Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr
 100 105 110

Lys Asn Leu Ile His Ile Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg
 115 120 125

Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp
 130 135 140

Val Thr Lys Ile Phe Ser Ser Glu Thr Asn Phe Ile Leu Glu Ile Cys
 145 150 155 160

Asp Asn Leu His Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met
 165 170 175

Asn Asn Glu Ser Ile Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu
 180 185 190

Val	Gln	Ser	His	Ala	Phe	Asn	Gly	Thr	Thr	Val	Ile	Ser	Leu	Val	Leu	195	200	205	
Lys	Glu	Asn	Val	His	Leu	Glu	Arg	Ile	His	Asn	Gly	Ala	Phe	Arg	Gly	210	215	220	
Ala	Thr	Gly	Pro	Ser	Ile	Leu	Asp	Ile	Ser	Ser	Thr	Lys	Leu	Gln	Ala	225	230	235	240
Leu	Pro	Ser	His	Gly	Leu	Glu	Ser	Ile	Gln	Thr	Leu	Ile	Ala	Thr	Ser	245	250	255	
Ser	Tyr	Ser	Leu	Lys	Lys	Leu	Pro	Ser	Arg	Glu	Lys	Phe	Ala	Asn	Leu	260	265	270	
Leu	Asp	Ala	Thr	Leu	Thr	Tyr	Pro	Ser	His	Cys	Cys	Ala	Phe	Arg	Asn	275	280	285	
Val	Pro	Thr	Lys	Asp	Tyr	Pro	Ala	Ile	Phe	Ala	Glu	Ser	Gly	Gln	Ser	290	295	300	
Gly	Trp	Asp	Tyr	Asp	Tyr	Gly	Phe	His	Leu	Pro	Lys	Thr	Pro	Arg	Cys	305	310	315	320
Ala	Pro	Glu	Pro	Asp	Ala	Phe	Asn	Pro	Cys	Glu	Asp	Ile	Met	Gly	Tyr	325	330	335	
Asp	Phe	Leu	Arg	Val	Leu	Ile	Trp	Leu	Ile	Asn	Ile	Leu	Ala	Ile	Met	340	345	350	
Gly	Asn	Met	Thr	Val	Leu	Phe	Val	Leu	Leu	Thr	Ser	Arg	Tyr	Lys	Leu	355	360	365	
Thr	Val	Pro	Arg	Phe	Leu	Met	Cys	Asn	Leu	Ser	Phe	Ala	Asp	Phe	Cys	370	375	380	
Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ile	Ala	Ser	Val	Asp	Ser	Gln	Thr	Lys	385	390	395	400
Gly	Gln	Tyr	Tyr	Asn	His	Ala	Ile	Asp	Trp	Gln	Thr	Gly	Ser	Gly	Cys	405	410	415	
Asn	Thr	Ala	Gly	Phe	Phe	Thr	Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr	420	425	430	
Thr	Leu	Thr	Val	Ile	Thr	Leu	Glu	Arg	Trp	His	Thr	Ile	Thr	Tyr	Ala	435	440	445	

Ile	His	Leu	Asp	Gln	Lys	Leu	Arg	Leu	Arg	His	Ala	Ile	Leu	Ile	Met	450	455	460
Leu	Gly	Gly	Trp	Leu	Phe	Ser	Ser	Leu	Ile	Ala	Met	Leu	Pro	Leu	Val	465	470	475 480
Gly	Val	Ser	Asn	Tyr	Met	Lys	Val	Ser	Ile	Cys	Leu	Pro	Met	His	Ile	485	490	495
Glu	Thr	Pro	Phe	Ser	Gln	Ala	Tyr	Val	Ile	Phe	Leu	Leu	Val	Leu	Asn	500	505	510
Val	Leu	Ala	Phe	Val	Ile	Ile	Cys	Ile	Cys	Tyr	Ile	Cys	Ile	Tyr	Phe	515	520	525
Thr	Val	Arg	Asn	Pro	Asn	Val	Ile	Ser	Ser	Asn	Ser	Asp	Thr	Lys	Ile	530	535	540
Ala	Lys	Lys	Met	Ala	Ile	Leu	Ile	Phe	Thr	Asp	Phe	Thr	Cys	Met	Ala	545	550	555 560
Pro	Ile	Ser	Phe	Phe	Ala	Ile	Ser	Ala	Ala	Phe	Lys	Met	Pro	Leu	Ile	565	570	575
Thr	Val	Thr	Asn	Ser	Lys	Val	Leu	Leu	Val	Leu	Phe	Tyr	Pro	Ile	Asn	580	585	590
Ser	Cys	Ala	Asn	Pro	Phe	Leu	Tyr	Ala	Ile	Phe	Thr	Lys	Thr	Phe	Arg	595	600	605
Arg	Asp	Phe	Phe	Leu	Leu	Leu	Gly	Lys	Phe	Gly	Cys	Cys	Lys	His	Arg	610	615	620
Ala	Glu	Leu	Tyr	Arg	Arg	Lys	Asp	Phe	Ser	Ala	Tyr	Thr	Ser	Asn	Tyr	625	630	635 640
Lys	Asn	Gly	Phe	Thr	Gly	Ser	Ser	Lys	Pro	Ser	Gln	Ser	Thr	Leu	Lys	645	650	655
Leu	Pro	Ala	Leu	His	Cys	Gln	Gly	Thr	Ala	Leu	Leu	Asp	Lys	Thr	Cys	660	665	670
Tyr	Lys	Glu	Tyr													675		

<210> 16

<211> 907
 <212> PRT
 <213> HUMAN

<400> 16

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
 1 5 10 15

Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
 20 25 30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
 35 40 45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
 50 55 60

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
 65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
 85 90 95

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
 100 105 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
 115 120 125

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
 130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
 145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
 165 170 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
 180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
 195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
 210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp

225		230		235		240
Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu						
	245		250		255	
Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile						
	260		265		270	
Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe						
	275		280		285	
Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu						
	290		295		300	
Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu						
305		310		315		320
Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr						
	325		330		335	
Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro						
	340		345		350	
Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro						
	355		360		365	
Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn						
	370		375		380	
Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu						
385		390		395		400
Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn						
	405		410		415	
Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn						
	420		425		430	
Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu						
	435		440		445	
Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn						
	450		455		460	
Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys						
465		470		475		480
Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn						

				485				490				495				
Lys	Gly	Asp	Asn	Ser	Ser	Met	Asp	Asp	Leu	His	Lys	Lys	Asp	Ala	Gly	
			500				505				510					
Met	Phe	Gln	Ala	Gln	Asp	Glu	Arg	Asp	Leu	Glu	Asp	Phe	Leu	Leu	Asp	
			515				520				525					
Phe	Glu	Glu	Asp	Leu	Lys	Ala	Leu	His	Ser	Val	Gln	Cys	Ser	Pro	Ser	
			530				535				540					
Pro	Gly	Pro	Phe	Lys	Pro	Cys	Glu	His	Leu	Leu	Asp	Gly	Trp	Leu	Ile	
545					550				555				560			
Arg	Ile	Gly	Val	Trp	Thr	Ile	Ala	Val	Leu	Ala	Leu	Thr	Cys	Asn	Ala	
			565				570				575					
Leu	Val	Thr	Ser	Thr	Val	Phe	Arg	Ser	Pro	Leu	Tyr	Ile	Ser	Pro	Ile	
			580				585				590					
Lys	Leu	Leu	Ile	Gly	Val	Ile	Ala	Ala	Val	Asn	Met	Leu	Thr	Gly	Val	
			595				600				605					
Ser	Ser	Ala	Val	Leu	Ala	Gly	Val	Asp	Ala	Phe	Thr	Phe	Gly	Ser	Phe	
			610				615				620					
Ala	Arg	His	Gly	Ala	Trp	Trp	Glu	Asn	Gly	Val	Gly	Cys	His	Val	Ile	
625					630				635				640			
Gly	Phe	Leu	Ser	Ile	Phe	Ala	Ser	Glu	Ser	Ser	Val	Phe	Leu	Leu	Thr	
			645				650				655					
Leu	Ala	Ala	Leu	Glu	Arg	Gly	Phe	Ser	Val	Lys	Tyr	Ser	Ala	Lys	Phe	
			660				665				670					
Glu	Thr	Lys	Ala	Pro	Phe	Ser	Ser	Leu	Lys	Val	Ile	Ile	Leu	Leu	Cys	
			675				680				685					
Ala	Leu	Leu	Ala	Leu	Thr	Met	Ala	Ala	Val	Pro	Leu	Leu	Gly	Gly	Ser	
			690				695				700					
Lys	Tyr	Gly	Ala	Ser	Pro	Leu	Cys	Leu	Pro	Leu	Pro	Phe	Gly	Glu	Pro	
705					710				715				720			
Ser	Thr	Met	Gly	Tyr	Met	Val	Ala	Leu	Ile	Leu	Leu	Asn	Ser	Leu	Cys	
			725				730				735					
Phe	Leu	Met	Met	Thr	Ile	Ala	Tyr	Thr	Lys	Leu	Tyr	Cys	Asn	Leu	Asp	

740	745	750
Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile		
755	760	765
Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe		
770	775	780
Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val		
785	790	795 800
Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn		
805	810	815
Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val		
820	825	830
Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser		
835	840	845
Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser		
850	855	860
Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu		
865	870	875 880
Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys		
885	890	895
His Leu Ser Ser Val Ala Phe Val Pro Cys Leu		
900	905	

<210> 17

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 17

Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys
1 5 10 15

<210> 18

<211> 22
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 18

Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met
1 5 10 15

Glu Ser Val Gln Cys Arg
20

<210> 19

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 19

Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly
1 5 10 15

Lys Arg Gln Thr Ser
20

<210> 20

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 20

Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
1 5 10 15

Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser
20 25 30

<210> 21
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21
Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe
1 5 10 15
Gly Arg Glu Val Ala Val Ala Asn Arg
20 25

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22
Arg Val Glu Ile Pro Asp Thr Met Thr Ser Trp
1 5 10

<210> 23
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23
Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln
1 5 10 15

Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile
20 25 30

Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys
35 40 45

Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val Ser
50 55 60

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GPCR21-F1
forward primer

<400> 24
tgtgttaagg ccacgctggt ag 22

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GPCR21-R1
reverse primer

<400> 25
tcactgtgat ggcaaggatg a 21

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 26
agccgagcca catcgct 17

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 27
gtgaccaggc gcccaatac 19

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 28
caaatccggt gactccgacc ttcacctt 28

<210> 29
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide 1

<220>
<221> modified_base
<222> (25)..(84)
<223> n=a or g or c or t; k=c or g or t

<400> 29
cgaagcgtaa gggcccagcc ggccnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
nnknnknnkn nknnknnknn knnkccgggt ccgggcggc 99

<210> 30

<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide 2

<220>
<221> modified_base
<222> (21)..(80)
<223> n=a or g or c or t; v=c or a or g

<400> 30
aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccgcccga cccgg 95

<210> 31
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 31
Pro Gly Pro Gly Gly
1 5

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 32
Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys Ile His
1 5 10

<210> 33
<211> 13

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

 <400> 33
 Cys Ile Arg His Ile Ser Arg Lys Ala Phe Phe Gly Leu
 1 5 10

 <210> 34
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

 <400> 34
 His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys
 1 5 10

 <210> 35
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

 <400> 35
 Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu
 1 5 10

 <210> 36
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 36
Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu
1 5 10

<210> 37
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37
Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38
Thr Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala
1 5 10

<210> 39
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39
Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 40
Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp
1 5 10

<210> 41
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41
Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys
1 5 10

<210> 42
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42
Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
1 5 10

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43

Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn
1 5 10

<210> 44

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 44

Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn
1 5 10

<210> 45

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 45

Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro
1 5 10

<210> 46

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 46

Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile
1 5 10

<210> 47

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 47

Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile
1 5 10

<210> 48

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48

Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala
1 5 10

<210> 49

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 49

Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys
1 5 10

<210> 50

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 50

Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser
1 5 10

<210> 51

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 51

Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr
1 5 10

<210> 52

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 52

Pro Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys Asn
1 5 10

<210> 53

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 53

Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys

1 5 10

<210> 54

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala

1 5 10 15

<210> 55

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala Leu Thr Gln Glu

1 5 10 15

<210> 56

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56

Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe

1 5 10 15

<210> 57

<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57
Ile Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe
1 5 10 15

<210> 58
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5'
primer

<400> 58
gcagcagcgg ccgcagaata tttgtctggg ttatagc 37

<210> 59
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3'
primer

<400> 59
gcagcagtcg acggaaactg gtttcattat actgtc 36

<210> 60
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 5'
primer

<400> 60

gcagcagcgg ccgcatgttc tttctacttc atttcatcg

39

<210> 61

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3' primer

<400> 61

gcagcagtcg acggttgtga gagtatagag cattgg

36